Chromosomal Localization of the Moloney Sarcoma Virus Mouse Cellular (c-mos) Sequence

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The Moloney sarcoma virus-specific *onc* gene, referred to as v-mos, was used as probe to hybridize to restricted DNAs from various mouse-Chinese hamster hybrid cell lines. These hybrid cells contain, in addition to all of the Chinese hamster chromosomes, various numbers (less than a full complement) of mouse chromosomes. Comparison of the presence or absence of the mouse cellular mos gene with the known karyotype in each of the hybrid cell lines allows us to conclude that the mos gene is on mouse chromosome 4.

The acute transforming retroviruses have acquired cellular sequences, called onc genes, that are responsible for their ability to cause rapid neoplastic transformation. onc genes are usually found in few or single copies in the host genome and are highly conserved among divergent animal species (3). The role of c-onc genes in normal cells is unknown, but it is presumed that they serve essential purposes since they have been conserved over long periods of evolutionary time. It is of interest to know the chromosomal location of the c-onc genes to determine (i) whether all of the known c-onc genes are linked on one chromosome or scattered throughout the genome: (ii) whether neighboring cellular genes are coordinately expressed during transformation; and (iii) the connection, if any, between known chromosomal aberrations in naturally occurring malignancies (12) and the location of c-onc genes. In this paper, we describe a series of experiments designed to identify the chromosomal location of the cellular homolog of the Moloney murine sarcoma virus (M-MSV) transforming gene (v-mos).

We used a nick-translated mos-specific probe isolated from a cellular DNA homolog (4, 17) to detect the corresponding c-mos sequence in DNA extracted from various mouse-Chinese hamster hybrid cell lines. The c-mos sequence is highly conserved among animal species (9), and we show that both Chinese hamster and mouse genomic DNA possess sequences homologous to the v-mos probe (Fig. 1, lanes 4 and 5, respectively). In SstI-digested genomic DNA, the Chinese hamster c-mos fragment is 4.3 kilobase pairs (kb) in size, and the mouse fragment is 6.0 kb (14). This enzyme was used to digest

genomic DNA from Chinese hamster-mouse hybrid cell lines (Fig. 1). The hybrid cell lines tested (Table 1) contained a full complement of Chinese hamster chromosomes, but they segregated various numbers of mouse chromosomes. Thus, v-mos hybridization to the hybrid cell DNA showed the presence of the hamster 4.3-kb fragment in every case. However, the 6.0-kb mouse fragment was absent in 4A6-4, EE1-1, ECm4e, and 132Az2 (Fig. 1, lanes 3, 8, 9, and 10) but was present in 2A1, 2A2, BEM1-6, and 6D3Az (Fig. 1, lanes 1, 2, 6, and 7). Comparison of the presence of the 6.0-kb fragment with the chromosome content of the hybrid cells shows complete concordance with the presence of mouse chromosome 4. Hybrid cell line 6D3Az (Fig. 1, lane 7) has only mouse chromosome 4 and still contains the mouse c-mos structural gene (Table 1). These results clearly demonstrate that the c-mos gene is present on mouse chromosome 4.

There are now more than 15 known viral onc genes (6). It will be of interest to see whether others are also genetically linked to the mouse chromosome 4. Other markers which map on chromosome 4 are the Friend virus 1 locus (Fv-I). This locus possesses a determinant for susceptibility to infection by murine retroviruses. The Fv-I locus has been shown to map within 0.6 centimorgans of hexose-6-phosphate dehydrogenase (Gpd-I) on mouse chromosome 4 (15, 16). It is not known, however, whether there is any connection between Fv-I and any of the known c-onc genes.

Tumor induction by retroviruses, in some cases at least, has been shown to result from retroviral insertion adjacent to a cellular onc

TABLE 1. Mouse chromosome content in hybrid cell lines tested for the presence of c-mosa

											Mouse chromosome no.	hromo	some 1	20.0								Hybridiza-
Lane	DNA	-	2	9	4	~	9	7	∞	6	91	=	12	13	41	15	15	17	18	19	×	tion to mos
-	2A1	62	85		38		20	69	27	58	35		81	4	62	11	73	8	19	69	4	+
7	2 A 2	23	8	22	43	7	69	69	33	\$	51		73	22	82	8	8	82	55	82	41	+
3	4A6-4	4	62				62	62								154	98		-	107	107	ı
4	Chinese	ł	I	ı	1	ı	ı	1	ı	ı	i	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı
	hamster																					
~	Mouse	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
9	BEM1-6	19	103	8	76		197^{d}	13	87	23	27		7	11	103	174	87	87	55	126	185^{d}	+
7	6D3Az				14																	+
œ	EE1-1		8						85				85					10	18			1
6	ECm4e														1004	1004						ı
10	132Az2		18					63								છ		1	154	754		1
			:	!			i			:	١.						<u>ا</u>					

^c Numbers indicate the mean number of copies of the chromosome per 100 cells control DNAs were run in lanes 4 and 5. The presence or absence of ^a Mouse chromosomes were identified by trypsin-Giemsa-Hoechst staining of metaphase spreads from hybrid cells. mouse chromosomes is indicated by + and -, respectively Lane number refers to lanes in Fig. 1

^d Includes copies of chromosomes present as translocations

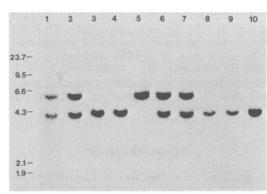


FIG. 1. Hybridization of a cloned c-mos probe to DNA from mouse-hamster hybrid cell lines. DNA was extracted from the cell lines identified in Table 1 and from mouse and hamster spleens. Molecular weights indicated on the left were obtained by running a HindIII digest of phage \(\lambda\) DNA. Hybrid cell DNA and mouse and hamster control DNAs were digested with SstI restriction endonuclease and electrophoresed on 1% agarose gels in 40 mM Tris-hydrochloride (pH 7.5)-20 mM sodium acetate-1 mM EDTA-0.5 µg of ethidium bromide per ml. DNA was transferred to diazobenzyloxymethyl paper (1) and hybridized to a nick-translated Aval-HindIII mos-specific fragment derived from pMS1 (4). Hybridization was performed at 42°C for 15 h in 50% formamide—5× SSC (1× SSC: 0.15 M NaCl plus 0.015 M sodium citrate)-0.1% Ficoll-0.1% bovine serum albumin-0.1% polyvinyl pyrrolidone-20 mM sodium phosphate (pH 6.5)-100 µg of sheared, denatured salmon sperm DNA per ml-10% sodium dextran sulfate-107 cpm of 32P-labeled mos probe per ml (labeled to ~700 cpm/pg). Filters were washed three times at room temperature in 0.1× SSC-0.1% SSC, then twice at 45°C in the same buffer. Bands indicate Chinese hamster DNA (lane 4); mouse DNA (lane 5); 2A1 (lane 1); 2A2 (lane 2); 4A6-4 (lane 3); BEM1-6 (lane 6); 6D3Az (lane 7); EE1-1 (lane 8); ECm4e (lane 9), and 132Az2 (lane 10).

gene (11, 13). Transcriptional control sequences supplied by the long terminal repeat sequences of the retrovirus effect higher levels of onc gene expression. It has also been demonstrated that cellular onc genes can be activated to cause cellular transformation by generating hybrids in vitro between a viral long terminal repeat sequence and the onc gene (4, 7).

It is not known how nonviral oncogenesis is initiated, but there is evidence that it is elicited by (i) mutations (2, 8); (ii) chromosomal rearrangements (12); or even (iii) reversible epigenetic events (5). T cell leukemias are induced by various agents, including Moloney leukemia virus, X rays, and chemical carcinogens (18), and all exhibit chromosomal abnormalities usually involving chromosomes 15, 12, and 6. Chromosome 4 has never been implicated in such aberrations.

754 NOTES J. VIROL.

Although many of the onc genes are expressed in normal cells, the mos gene-specific RNA has never been detected in normal or transformed cells other than in M-MSV-transformed cells (10). By identifying the chromosomal locus, it may be possible, by identifying adjacent genes and their functions, to ascertain a normal cell function for mos.

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